

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:17:05 ; Search time 17.21 Seconds

(without alignments)
112.588 Million cell updates/sec

Title: US-09-331-631A-22_COPY_25_84

Perfect score: 350
Sequence: 1 EDNNHHHGGHKSQCVRRC.....EKRRKSRHEADRDGSGSS 60

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	346	98.9	573	1	GLBL_MAIZE
2	81.5	23.3	605	1	VCLA_GOSHI
3	78	22.3	494	1	SFR4_GOSHI
4	71	20.3	699	1	SRCH_HUMAN
5	69.5	19.9	241	1	Y087_CAEEL
6	69	19.7	407	1	IE68_HVSA
7	69	19.7	588	1	VCLA_GOSHI
8	68.5	19.6	1407	1	TRHY_RABIT
9	67.5	19.3	466	1	CYP8_CAEEL
10	66	18.9	2339	1	CCAB_HUMAN
11	66	18.9	2339	1	CCAB_RABIT
12	65.5	18.7	345	1	VU79_HSV62
13	65.5	18.7	520	1	ITSN_HUMAN
14	65.5	18.7	2222	1	CCAE_RAT
15	65.5	18.7	2272	1	CCAE_MOUSE
16	65.5	18.7	2312	1	CCAE_MOUSE
17	65	18.6	107	1	HSP2_MOUSE
18	65	18.6	1130	1	REPT_MOUSE
19	63.5	18.1	520	1	LEG2_PEA
20	63.5	18.1	2505	1	CCAA_HUMAN
21	63	18.0	311	1	OSTP_RABIT
22	63	18.0	330	1	RLX3_STAU
23	63	18.0	344	1	SFR6_HUMAN
24	63	18.0	380	1	RDP_HUMAN
25	63	18.0	467	1	RXRG_CHICK
26	63	18.0	632	1	CCB2_RABIT
27	63	18.0	747	1	TRIS_ECOLI
28	62.5	17.9	103	1	HSP2_MACNE
29	62.5	17.9	517	1	LEGA_PEA
30	62.5	17.9	520	1	GAG_HV28
31	62	17.7	524	1	SBP_SOYBN
32	62	17.7	623	1	PNT1_DROME
33	62	17.7	654	1	CIK4_MUSPF

34	62	17.7	852	1	SRCH_RABIT	P16230 oryctolagus
35	62	17.7	1549	1	TRHY_SHEEP	P22793 ovis aries
36	61.5	17.6	522	1	GAG_HV261	P18041 human immun
37	61.5	17.6	550	1	BLSA_HUMAN	O02832 homo sapien
38	61.5	17.6	1234	1	CPAH_MOUSE	P06909 mus musculu
39	61	17.4	617	1	YACH_ECOLI	P36682 escherichia
40	61	17.4	1097	1	CCT_DROME	O96433 drosophila
41	61	17.4	1898	1	TRHY_HUMAN	O07283 homo sapien
42	61	17.4	2327	1	CCAB_MOUSE	O55017 mus musculu
43	60.5	17.3	33	1	MBPL_MAIZE	P28794 zea mays (m
44	60.5	17.3	195	1	AANT_HDVS1	P25883 hepatitis d
45	60.5	17.3	195	1	AANT_HDVS2	P25884 hepatitis d

ALIGNMENTS

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RESULT 1
GLBL_MAIZE STANDARD; PRT: 573 AA.
AC P15590;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE GLOBULIN-1 S ALLELE PRECURSOR (GLBL-S) (7S-LIKE).
GN GBL1.
OS zea mays (Maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. INBRED LINE VA26;
RA Belanger F.C., Kriz A.L.;
RT "Molecular characterization of the major maize embryo globulin encoded
RT by the Gbl1 gene."
RL Plant Physiol. 91:656-643(1989).
RN [2]
RP SEQUENCE OF 87-100.
RX MEDLINE=89374022; PubMed=2775172;
RA Kriz A.L.;
RT "Characterization of embryo globulins encoded by the maize Glb
RT genes."
RL Biochem. Genet. 27:239-251(1989).
CC -I- PPM: THREE PROTEIN-PROCESSING STEPS OCCUR IN THE FORMATION OF THE
CC MATURE PROTEIN FROM THE PRIMARY TRANSLATION PRODUCT.
CC -I- POLYMORPHISM: THE THREE MOST COMMONLY OCCURRING GBL1 ALLELES HAVE
CC THE DESIGNATION L, I, AND S FOR LARGE, INTERMEDIATE, AND SMALL
CC PROTEINS, RESPECTIVELY.
CC -I- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
CC CONVICILIN, CONGLICININ, ETC.).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M24845; AAA33467.1; -.
DR HSSP; P50477; ICAM.
DR MAIZEEDB; 30181; -.
DR INTERPRO; IPR001113; -.
DR PRAM; PF00546; Seedstore_7s; 1.
KW Seed storage protein; Signal.
FT SIGNAL 1 18 OR 21 (POTENTIAL).
FT PROPEP 19 86
FT CHAIN 87 573 GLOBULIN-1 S ALLELE.
FT CARBOHYD 349 349 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 573 AA: 65029 MW: 525ED1DD0A062976 CRC64;
Query Match 98.9%; Score 346; DB 1; Length 573;

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RT protein, and localization of the gene to human chromosome 19 and
RL mouse chromosome 7.
CC Genomics 9:656-669(1991).
CC -1- FUNCTION: HEP MAY PLAY A ROLE IN THE REGULATION OF CA(2+)
CC SEQUESTRATION OR RELEASE IN THE SR OF SKELETAL AND CARDIAC
CC MUSCLE.
CC -1- SUBCELLULAR LOCATION: SARCOPLASMIC RETICULUM LUMEN.
CC -1- SIMILARITY: STRONG, TO RABBIT HRC.
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CC -----
DR EMBL: M60052; AAA88071.1; -.
DR MIM: 142705; -.
KW Calcium-binding; Signal; Repeat; Polymorphism.
FT SIGNAL 1 28
FT CHAIN 29 699
FT FT SARCOPASMIC RETICULUM HISTIDINE-RICH
FT FT CALCIUM-BINDING PROTEIN.
FT FT GLU-RICH (ACIDIC).
FT FT ASP-RICH (ACIDIC).
FT FT 4 X TANDEM REPEATS, ACIDIC.
FT FT 1-1.
FT FT 1-2.
FT FT 1-3.
FT FT 1-4.
FT FT 6 X APPROXIMATE TANDEM REPEATS.
FT FT 2-1.
FT FT 2-2.
FT FT 2-3.
FT FT 2-4.
FT FT 2-5.
FT FT 2-6.
FT FT METAL-BINDING (POTENTIAL).
FT FT S -> V.
FT FT VARIANT 96
FT FT /FTID=VAR_005623.
SQ SEQUENCE 699 AA; 80244 MW; 9922EEDF012C61DD CRC64;

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Query Match 20.3%; Score 71; DB 1; Length 699;
 Best Local Similarity 24.2%; Pred. No. 3.5;
 Matches 22; Conservative 7; Mismatches 28; Indels 34; Gaps 3;

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OY 1 EDNNHHNG-----GHS-----GCVRRCEDRPMH----- 26
DB 413 EVPHNNHVRPEDEVSALGHAQPSHROSDDETGHGQSGSIKEMSHNPRGHTVVK 472
OY 27 QRPRLCEQREERKROERSHNEADDRSGE 57
DB 473 DRSHLRKDDSEERKEKEDPSHEEDDESS 503

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RESULT 5
 Y087_CAEEL STANDARD; PRT; 241 AA.
 AC P34623;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE HYPOTHEICAL 28.5 KDA PROTEIN ZK1236.7 IN CHROMOSOME III.
 GN ZK1236.7
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; Pubmed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

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RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Lattelle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Riken L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterson P., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Mohlman R.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
CC -----
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CC -----
DR EMBL: L13200; AAA28188.1; -.
DR PIR: S44893; S44893.
DR WORMPEP: ZK1236.7; CE00384.
KW Hypothetical protein.
SQ SEQUENCE 241 AA; 28541 MW; 610ECA6537159FA7 CRC64;

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Query Match 19.9%; Score 69.5; DB 1; Length 241;
 Best Local Similarity 41.9%; Pred. No. 1.9;
 Matches 18; Conservative 9; Mismatches 9; Indels 7; Gaps 2;

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OY 17 VRCEDRPMHQRPCLEQREERERK--QERSHNEADDRSGE 57
DB 65 MREYEVREERERK---REERERKDEERAREADEAKAE 102

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RESULT 6
 IE68_HSVSA STANDARD; PRT; 407 AA.
 AC Q01042;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE IMMEDIATE-EARLY PROTEIN.
 GN 73 OR ECLF1.
 OS Herpesvirus saimiri (strain 11).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92333686; Pubmed=1321287;
 RA Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
 RA Newman C., Wiltman S., Craxton M.A., Coleman H., Fleckenstein B.,
 RA Honess R.W.;
 RT "Primary structure of the herpesvirus saimiri genome.";
 RL J. Virol. 66:5047-5058(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92230228; Pubmed=1314457;
 RA Nicholas J., Cameron K.R., Coleman H., Newman C., Honess R.W.;
 RT "Analysis of nucleotide sequence of the rightmost 43 kbp of
 RT herpesvirus saimiri (HVS) L-DNA: general conservation of genetic
 RT organization between HVS and Epstein-Barr virus.";
 RL Virology 188:296-310(1992).
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-1 AND
 CC HSV-2 IE-68 (US1), EBV-1 65, EBV-4 (ORF4), PRV RSP40, AND VZV 63.
 CC -----
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CC -----
DR EMBL; X64346; CAA45696.1; -
DR EMBL; M86409; AAA46149.1; -
DR EMBL; S76368; AAB21116.1; -
DR PIR; G36813; EDBE03.
DR PIR; S20244; S20244.
DR HSSP; P53041; 1A17.
DR Early protein.
FT DOMAIN 60
SQ SEQUENCE 407 AA; 46617 MW; FFD399CAB2CE136C CRC64;
GLU-RICH (ACIDIC).

Query Match 19.7%; Score 69; DB 1; Length 407;
Best Local Similarity 45.7%; Pred. No. 3.4;
Matches 16; Conservative 5; Mismatches 12; Indels 2; Gaps 1.

OY 26 HORPRCL--ECQREEREKROERSHEDDRSGEG 58
II: I II III : II I : I II
DB 52 HQOQALTEQREEREVEEGEERERRERGEEREGC 86

RESULT 7
VCLB_GOSHI STANDARD; PRT; 588 AA.
ID VCLB_GOSHI
AC P09801;
AT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VICILIN C72 PRECURSOR (ALPHA-GLOBULIN B).
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Malvales; Malvaceae; Gossypium.
RN [1]
RP SEQUENCE FROM N.A.
RA Chlan C.A., Pyle J.B., Legocki A.B., Dure L. III;
RT "developmental biochemistry of cottonseed embryogenesis and
RT germination. XVIII. cDNA and amino acid sequences of the members of
RT the storage protein families.";
RL Plant Mol. Biol. 7:475-489(1986).
CC -1- FUNCTION: SEED STORAGE PROTEIN.
CC -1- SUBCELLULAR LOCATION: CYTOSOL; MEMBRANE-BOUND VACUOLAR PROTEIN
CC BODIES.
CC -1- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
CC CONVICILIN, CONLYCININ, ETC.).
CC -----
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CC -----
DR EMBL; M16891; AAA33071.1; -
DR PIR; A30838; FMCNAB.
DR HSSP; P50477; ICAX.
DR INTERPRO: IPR001113; -
DR PRAM; PF00546; Seedstore_7s; 1.
DR Seed storage protein; Signal.
FT SIGNAL 1
FT CHAIN 25
SQ SEQUENCE 588 AA; 69729 MW; 63E695B29AB8ADDB CRC64;
VICILIN C72.

Query Match 19.7%; Score 69; DB 1; Length 588;
Best Local Similarity 30.6%; Pred. No. 4.7;
Matches 15; Conservative 12; Mismatches 16; Indels 6; Gaps 3;

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DB      126 ECGQHCHQGEGR-ERKQOCVRECHERGQENWRREREAEDEETEGC 173
          : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
RESULT# 8
ID       TRHY_RABIT STANDARD: PRT: 1407 AA.
AC       P37709:
DT       01-OCT-1994 (Rel. 30, Created)
DT       01-OCT-1994 (Rel. 30, Last sequence update)
DT       01-OCT-2000 (Rel. 40, Last annotation update)
DE       TRICHOHYALIN.
GN       THH.
OS       Oryctolagus cuniculus (Rabbit).
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC       Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN       [1]
RP       SEQUENCE FROM N.A.
RA       Fietz M.J., Rogers G.E.;
RL       submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
CC       -I- FUNCTION: INTERMEDIATE FILAMENT ASSOCIATED PROTEIN THAT ASSOCIATES
           IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE
           INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR
           LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY
           ISODIEPLETIC BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER
           WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN
           ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN
           ITS OWN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DURING TERMINAL
           DIFFERENTIATION.
CC       -I- SUBUNIT: HOMODIMER (PROBABLE).
CC       -I- TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES SUCH AS
           THE INNER ROOT SHEATH (IRS) OF HAIR FOLLICLES AND MEDULLA, AND IN
           THE FLILIFORM PAPILLAE OF DORSAL TONGUE EPITHELIUM (PROBABLE).
CC       -I- DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION OF
           THE EPIDERMIS.
CC       -I- DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND
           CALCIUM-BINDING DOMAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST
           ENTIRELY ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REPEATS
           OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRAINED
           ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 5 IS
           THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS.
           DOMAINS 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN
           THE MOLECULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG
           DIFFERENT SPECIES.
CC       -I- PTM: KNOWN SUBSTRATE OF TRANSGUTAMINASE. SOME 200 ARGINES ARE
           PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE.
CC       -I- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S-100
           FAMILY.
CC       -I- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
-----
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           CC
DR       EMBL: Z19092; CAI79519.1; -.
DR       PIR: S28589; S28589.
DR       HSSP: P02633; IBQC.
DR       INTERPRO: IPR001751; -.
DR       INTERPRO: IPR002048; -.
DR       Pfam: PF01023; S.100; 1.
DR       Pfam: PF00036; efhand; 1.
DR       ProSITE: PS00018; EF_HAND_1.
DR       ProSITE: PS00303; S100_CABP; 1.
KM       Repeat: Calcium-binding.
FT       DOMAIN 1 91 S-100 LIKE.
FT       CA_BIND 22 33 SITE I (LOW AFFINITY) (POTENTIAL).
FT       CA_BIND 62 73 SITE II (HIGH AFFINITY) (POTENTIAL).
FT       CA_BIND 1407 AA: AEI7DZA159F12BTF CRG64.
SEQUENCE

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BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
ATP (POTENTIAL).
CALCIUM ION SELECTIVITY AND PERMEABILITY

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FT FT SITE 663 663 (BY SIMILARITY).
FT FT SITE 1365 1365 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT FT SITE 1655 1655 (BY SIMILARITY).
FT FT SITE 1655 1655 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT FT MOD_RES 1719 1719 (BY SIMILARITY).
FT FT CAL_BIND 1737 1748 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT FT CARBOHYD 236 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 1563 1663 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 1675 1675 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT VARSPLIC 2164 2339 GSGSVNCSPLSTSGASTPGRGRRQLPPPLPRRSITYK
FT TANSPLHFGAQRSLPAESPGRLSGLSLSEHNALDRLDLS
FT QPLAPGRISGADPYLIGORDSEASVHSLSEHNALDRLDLS
FT NSGRSRSTYVSLTSGHPLRRVPCNYCTGLSSGGRAR
FT HSYHHPODHWC -> AGSAVGRPNTPPCRTPSPASPMPL
FT ALLEALTLTWGSWYTVARPLSTPCLRRTRSLRRLMPTRAAP
FT PGLDTCP (IN ISOFORM ALPHA-1B-2).
SQ SEQUENCE 2339 AA; 262494 MW; 17A456D1E76B39D CRC64;

Query Match 18.9%; Score 66; DB 1; Length 2339;
Best Local Similarity 28.2%; Pred. No. 32;
Matches 24; Conservative 7; Mismatches 14; Indels 40; Gaps 5

OY 4 NHHHGHKSGQVCRCEDRPWHPRCLEO-----C 35
Db 2050 HHHHH-----RCHRR-RDR-----KQSLSEKGSLSLMDHGPASSAVGCLPPGEGPTGC 2098
OY 36 REERERKROERSRHEADRSGEGSS 60
Db 2099 R-REERERROERGSRQERRRPPSSSS 2122

RESULT 11
CCAB_RABIT STANDARD; PRT; 2339 AA.
AC 003152;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM
DE CHANNEL, L-TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL
DE I11) (B111).
GN CACNA1B OR CACNL1A5 OR CACN5.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=93236885; Pubmed=8386525;
RA Fujita Y., Mylnieff M., Dirksen R.T., Kim M.-S., Nildome T., Nakai J.,
RA Friedrich T., Tawbe N., Miyata T., Furutachi T., Furutani D.,
RA Mikoshiba K., Mori Y., Beam K.G.;
RT "Primary structure and functional expression of the omega-conotoxin-
RT sensitive N-type calcium channel from rabbit brain.";
RL Neuron 10:585-598(1993).
CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B
CC GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS
CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
CC BY OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND BY OMEGA-AGATOXIN-
CC I11A (OMEGA-AGA-I11A). THEY ARE HOWEVER INSENSITIVE TO
CC DIHYDROPYRIDINES (DHP), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
CC CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN
CC DIRECTED MIGRATION OF IMMATURE NEURONS.
CC -!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS

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	CC	IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-	
	CC	-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS	
	CC	SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM	
	CC	CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/Delta	
	CC	LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.	
	CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.	
	CC	-1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION THROUGHOUT THE BRAIN,	
	CC	HIGHEST LEVELS IN CORPUS STRIATUM AND MIDBRAIN.	
	CC	-1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE	
	CC	HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE	
	CC	POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS	
	CC	PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A	
	CC	SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.	
	CC	-1- PTM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAKP, PKC AND GSKP	
	CC	(BY SIMILARITY).	
	CC	-1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS	
	CC	FAMILY.	
	CC	-----	
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	CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -	
	CC	the European Bioinformatics Institute. There are no restrictions on its	
	CC	use by non-profit institutions as long as their content is in no way	
	CC	modified and this statement is not removed. Usage by and for commercial	
	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
	CC	or send an email to license@isb-sib.ch).	
	CC	-----	
	DR	EMBL; D14157; BAA03202.1; -.	
	DR	INTERPRO; IPR000636; -.	
	DR	INTERPRO; IPR002077; -.	
	DR	Pfam; PF005520; Ion.trans; 4.	
	DR	PRINTS; PR00167; CACCHANNEL.	
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;		
KW	Calcium channel; Glycoprotein; Repeat; Multigene family;		
MZ	Calciun-binding; Phosphorylation; ATP-binding.		
FT	REPEAT	82	359
FT	REPEAT	469	713
FT	REPEAT	1142	1424
FT	REPEAT	1461	1714
FT	DOMAIN	1	95
FT	TRANSSEM	96	114
FT	DOMAIN	115	132
FT	TRANSSEM	133	152
FT	DOMAIN	153	163
FT	TRANSSEM	164	183
FT	DOMAIN	184	187
FT	TRANSSEM	188	206
FT	DOMAIN	207	225
FT	TRANSSEM	226	245
FT	DOMAIN	246	331
FT	TRANSSEM	332	356
FT	DOMAIN	357	483
FT	TRANSSEM	484	502
FT	DOMAIN	503	517
FT	TRANSSEM	518	537
FT	DOMAIN	538	545
FT	TRANSSEM	546	563
FT	DOMAIN	564	574
FT	TRANSSEM	575	593
FT	DOMAIN	594	612
FT	TRANSSEM	613	632
FT	DOMAIN	633	683
FT	TRANSSEM	686	710
FT	DOMAIN	711	1156
FT	TRANSSEM	1157	1174
FT	DOMAIN	1175	1190
FT	TRANSSEM	1191	1210
FT	DOMAIN	1211	1222
FT	TRANSSEM	1223	1241
FT	DOMAIN	1242	1250
FT	TRANSSEM	1252	1271
FT	DOMAIN	1271	1289
FT	TRANSSEM	1290	1309
FT	DOMAIN	1310	1396

FT	TRANSMEM	1397	1421	S6 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1422	1476	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1477	1495	S1 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1496	1510	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1511	1530	S2 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1531	1538	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1539	1557	S3 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1558	1566	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1567	1585	S4 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1586	1604	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1605	1624	S5 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1625	1686	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1687	1711	S6 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1712	2339	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	2051	2055	POLY-HIS.
FT	DOMAIN	2119	2123	POLY-SER.
FT	DOMAIN	2319	2324	POLY-GLY.
FT	DOMAIN	379	396	BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT	NP BIND	452	459	APP (POTENTIAL).
FT	SITE	314	314	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	663	663	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1370	1370	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1658	1658	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	MOD_RES	1722	1722	PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT	CA BIND	1740	1751	BY SIMILARITY.
FT	CARBOHYD	256	256	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1566	1566	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1678	1678	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	2339	AA: 261178	MM: 040130d93794c8b834 CRC64;

[illegible]

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 CC or send an email to license@isb-sib.ch).

DR EMBL: L14772; AAB06363.1; -
 DR MIM: 602442; -
 DR INTERPRO: IPR001452; -

Query Match 18.7%; Score 65.5; DB 1; Length 345;
 Best Local Similarity 26.4%; Pred. No. 6.5;
 Matches 14; Conservative 14; Mismatches 14; Indels 11; Gaps 2;

QY 2 DDHHHHGKSGOCVRCEDRPWQHQRCLDCCREERERKROERSHEDDR 54
 DB 161 DDEHRRKSGKQKER--RKVED-----IDKKKEDEKRRKQEKRRNDEDKR 202

RESULT 13

ITSN_HUMAN STANDARD; PRT; 520 AA.

AC 015811;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERSECTIN (SH3 DOMAIN-CONTAINING PROTEIN SH3P17).
 GN ITSN OR SH3D1A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 [1]

RP SEQUENCE FROM N.A.
 RC TISSUE-BONE MARROW;
 RX MEDLINE=98294438; PubMed=9630982;
 RA Sparks A.B., Hoffman N.G., McConnell S.J., Fowlkes D.M., Kay B.K.;
 RT "Cloning of ligand targets: systematic isolation of SH3 domain-
 RT containing proteins."
 RL Nat. Biotechnol. 14:741-744(1996).
 RN [2]

RP GENE MAPPING.
 RX MEDLINE=98127038; PubMed=9465890;
 RA Chen H., Antonarakis S.E.;
 RT "The SH3D1A gene maps to human chromosome 21q22.1-->q22.2."
 CC Cytogenet. Cell Genet. 78:213-215(1997).
 CC -1- SIMILARITY: CONTAINS 4 SH3 DOMAINS.

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 CC or send an email to license@isb-sib.ch).

DR EMBL: U61166; AAC50592.1; -
 DR HSSP: P29354; IGFID.
 DR MIM: 602442; -

DR INTERPRO: IPR001452; -
 DR PFAM: PF00018; SH3; 4.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PROSITE: PS00002; SH3; 4.

KW SH3 domain; Repeat. 177
 FT DOMAIN 116 177 SH3.
 FT 284 342 SH3.
 FT DOMAIN 374 514 SH3.
 FT 455 SH3.
 SEQUENCE 520 AA; 57976 MW; 614043F1DB096C60 CRC64;

Query Match 18.7%; Score 65.5; DB 1; Length 520;
 Best Local Similarity 33.9%; Pred. No. 9.4;
 Matches 19; Conservative 9; Mismatches 11; Indels 17; Gaps 4;

QY 18 RRCR--DRPW-----HQRPRCL--EQCREERERK--QERSRHEDDRSG 56
 DB 27 RRAQRDKQLVHVOEDEHQRPRKLEERKLRRESVKKDEKQKQDEADKLG 82

RESULT 14

CCAE RAT STANDARD; PRT; 2222 AA.

AC 007652;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE VOLTAGE-DEPENDENT R-TYPE CALCIUM CHANNEL ALPHA-1E SUBUNIT (CALCIUM
 DE CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE, ISOFORM 6) (RBE-11) (RBE2)
 GN (BRAIN CALCIUM CHANNEL II) (B11).
 GN CACNA1E OR CACNL1A6 OR CACHE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
 RX MEDLINE=93262464; PubMed=838125;
 RA Soong T.W., Stea A., Hodson C.D., Dubel S.J., Vincent S.R.,
 RA Snutch T.P.;
 RT "Structure and functional expression of a member of the low voltage-
 RT activated calcium channel family."
 RL Science 260:1133-1136(1993).

CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E
 CC BELONGS TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
 CC BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA).
 CC THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), OMEGA-
 CC CONOTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-
 CC AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1E SUBUNIT COULD BE
 CC INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS
 CC IMPORTANT FOR INFORMATION PROCESSING.

CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
 CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
 CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE POR-
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN CENTRAL NERVOUS SYSTEM AND IN
 CC INSULINOMA.
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 CC FAMILY.

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 CC or send an email to license@isb-sib.ch).

DR EMBL: L15453; AAA0855.1; -
 DR INTERPRO: IPR000636; -

DR INTERPRO: IPR002077; .
 DR PRAM; Pf00520; Ion_trans; 4.
 DR PRINTS; PR00167; CACHTANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation.
 FT REPEAT 27 305 I.
 FT REPEAT 413 657 II.
 FT REPEAT 1092 1378 III.
 FT REPEAT 1415 1678 IV.
 FT DOMAIN 1 40 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 41 59 S1 OF REPEAT I (POTENTIAL).
 FT DOMAIN 60 78 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 79 97 S2 OF REPEAT I (POTENTIAL).
 FT DOMAIN 98 109 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 110 124 S3 OF REPEAT I (POTENTIAL).
 FT DOMAIN 125 136 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 137 156 S4 OF REPEAT I (POTENTIAL).
 FT DOMAIN 157 174 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 175 195 S5 OF REPEAT I (POTENTIAL).
 FT DOMAIN 196 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 278 301 S6 OF REPEAT I (POTENTIAL).
 FT DOMAIN 302 427 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 428 447 S1 OF REPEAT II (POTENTIAL).
 FT DOMAIN 448 460 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 461 480 S2 OF REPEAT II (POTENTIAL).
 FT DOMAIN 481 489 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 490 508 S3 OF REPEAT II (POTENTIAL).
 FT DOMAIN 509 518 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 519 537 S4 OF REPEAT II (POTENTIAL).
 FT DOMAIN 538 556 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 557 576 S5 OF REPEAT II (POTENTIAL).
 FT DOMAIN 577 629 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 630 654 S6 OF REPEAT II (POTENTIAL).
 FT DOMAIN 655 1100 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 1101 1117 S1 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1118 1141 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 1142 1161 S2 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1162 1169 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 1170 1192 S3 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1193 1206 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 1207 1224 S4 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1225 1243 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 1244 1263 S5 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1264 1350 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 1351 1374 S6 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1375 1431 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 1432 1450 S1 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1451 1467 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 1468 1485 S2 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1486 1493 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 1494 1512 S3 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1513 1523 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 1524 1542 S4 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1543 1561 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 1562 1581 S5 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1582 1650 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 1651 1676 S6 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1677 2222 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 667 672 POLY-GLU.
 FT DOMAIN 699 704 POLY-ARG.
 FT TRANSSEM 718 723 POLY-ARG.
 FT DOMAIN 1058 1064 POLY-GLU.
 FT TRANSSEM 1180 1183 POLY-VAL.
 FT DOMAIN 2193 2196 POLY-ARG.
 FT TRANSSEM 325 342 BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
 FT SITE 260 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
 FT SITE 608 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
 FT SITE 1324 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).

FT SITE 1615 1615 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
 FT CA_BIND 377 389 BY SIMILARITY.
 FT MOD_RES 1686 1686 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT CA_BIND 1704 1715 BY SIMILARITY.
 FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1518 1518 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1523 1523 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1641 1641 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 2222 AA; 252114 MW; DP6452A2175CEB19 CMC64;
 Query Match 18.7%; Score 65.5; DB 1; Length 2222;
 Best Local Similarity 32.4%; Pred. No. 34;
 Matches 23; Conservative 9; Mismatches 24; Indels 15; Gaps 4;
 QY 3 DNHHHGHKSGQCV-RCEDRPWHQRPCLCEGCEER-----EKROERS---R 48
 DB 1977 DSGHKSPTHRSGRGERSKERK-HLSPDVSRCSERGTQADWESPERSKPSSEGR 2035
 OY 49 HEADRSGEGS 59
 DB 2036 SQTPNRGCTGS 2046
 RESULT 15
 CCAL_MOUSE STANDARD; PRT; 2272 AA.
 ID CCAL_MOUSE
 AC 061250;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE VOLTAGE-DEPENDENT R-TYPE CALCIUM CHANNEL ALPHA-1E SUBUNIT (CALCIUM CHANNEL, L TYPE; ALPHA-1 POLYPEPTIDE, ISOFORM 6) (BRAIN CALCIUM CHANNEL, II) (B11)
 DE CACNAIE OR CCHRA1 OR CACNM1A6 OR CACHE6.
 GN Mus musculus (mouse).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE=94350992; PubMed=8071363;
 RA Williams M.E., Marubio L.M., Deal C.R., Hans M., Brust P.F., Philipson L.H., Miller R.J., Johnson E.C., Harpold M.M., Ellis S.B.;
 RT "Structure and functional characterization of neuronal alpha 1E calcium channel subtypes.";
 RL J. Biol. Chem. 269:22347-22357(1994).
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-ITIA (OMEGA-AGA-ITIA). THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1E SUBUNIT COULD BE INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS IMPORTANT FOR INFORMATION PROCESSING.
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNTS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNTS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURONAL TISSUES, RETINA, SPLEEN, AND PANCREATIC ISLET CELLS.
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE

